

SEQUENCE LISTING

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<110> NAYLOR, STUART
      KINGSMAN, SUSAN MARY
      BINLEY, KATIE
<120> POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
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<140> 10/810,262
<141> 2004-03-26
<150> 09/787,562
<151> 2001-07-06
<150> PCT/GB99/03181
<151> 1999-09-22
<150> PCT/GB98/02885
<151> 1998-09-23
<150> GB 9901906.9
<151> 1999-01-28
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<151> 1999-02-16
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oligonucleotide

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ccatagtccc gcccctaact ccgcccatcc cgcccctaac tccgcccagt tccgcccatt 180
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gtcgtgcagg acgtgacatc tagagaacca tcagatgttt ccagggtgcc ccaaggacct 120
gaaatgaccc tgtgccttat ttgaactaac caatcagttc gcttctcgct tctgttcgcg 180
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gccctgaaca gcccctgag cggcgcatg cgcggcatca ggggcgctga cttccagtgc 180
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tggccccaga agagcgtgtg gcacggctcc gaccccaacg gccgcaggct gaccgagagc 480
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	aag Lys 210	tag														633
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Phe	Gln	Pro 35	Val	Leu	His	Leu	Val 40	Ala	Leu	Asn	Ser	Pro 45	Leu	Ser	Gly	
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Arg 65	Ala	Val	Gly	Leu	Ala 70	Gly	Thr	Phe	Arg	Ala 75	Phe	Leu	Ser	Ser	Arg 80	
Leu	Gln	Asp	Leu	Tyr 85	Ser	Ile	Val	Arg	Arg 90	Ala	Asp	Arg	Ala	Ala 95	Val	
Pro	Ile	Val	Asn 100	Leu	Lys	Asp	Glu	Leu 105	Leu	Phe	Pro	Ser	Trp 110	Glu	Ala	
Leu	Phe	Ser 115	Gly	Ser	Glu	Gly	Pro 120	Leu	Lys	Pro	Gly	Ala 125	Arg	Ile	Phe	
		_	_	_	_			_		Pro		-	Pro	Gln	Lys	
Ser 145	Val	Trp	His	Gly	Ser 150	Asp	Pro	Asn	Gly	Arg 155	Arg	Leu	Thr	Glu	Ser 160	
Tyr	Cys	Glu	Thr	Trp 165	Arg	Thr	Glu	Ala	Pro 170	Ser	Ala	Thr	Gly	Gln 175	Ala	
Ser	Ser	Leu	Leu 180	Gly	Gly	Arg	Leu	Leu 185	Gly	Gln	Ser	Ala	Ala 190	Ser	Сув	

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ggcaacggca agaactacag gggcaccatg agcaagacca agaacggcat cacctgccag 180
aagtggagca gcaccagccc ccacaggcct cgcttcagcc ccgccaccca ccccagcgag 240
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accaccgacc ctgagaagcg ctacgactac tgcgacatcc tggagtgcga ggaagagtgt 360
atgcactgca gcggggagaa ctacgacggc aagatcagca agaccatgag cggcctggag 420
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ccacccagca geggeeccac etaccagtge etgaagggea eeggegagaa ttacegegge 660
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acceacaace geaceeega gaactteeee tgeaagaace tegaegagaa ttattgeegg 780
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gca gtc ttc gtt tcg ccc agc ggt acc gga tcc tta ttt gaa aag aaa
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Ala Val Phe Val Ser Pro Ser Gly Thr Gly Ser Leu Phe Glu Lys Lys
gtg tat ctc tca gag tgc aag act ggg aat gga aag aac tac aga ggg
                                                                   144
Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly
acg atg tcc aaa aca aaa aat ggc atc acc tgt caa aaa tgg agt tcc
Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser
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					tac Tyr	_				_		_	_	_		288
					act Thr											336
					gag Glu											384
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gac Asp 145	tct Ser	cag Gln	agc Ser	cca Pro	cac His 150	gct Ala	cat His	gga Gly	tac Tyr	att Ile 155	cct Pro	tcc Ser	aaa Lys	ttt Phe	cca Pro 160	480
					aag Lys											528
					acc Thr											576
					aca Thr											624
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aac Asn	tac Tyr	tgc Cys	cgc Arg 260	aat Asn	cct Pro	gac Asp	gga Gly	aaa Lys 265	agg Arg	gcc Ala	cca Pro	tgg Trp	tgc Cys 270	cat His	aca Thr	816
acc Thr	aac Asn	agc Ser 275	caa Gln	gtg Val	cgg Arg	tgg Trp	gag Glu 280	tac Tyr	tgt Cys	aag Lys	ata Ile	ccg Pro 285	tcc Ser	tgt Cys	gac Asp	864

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Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly
35 40 45

Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser 50 60

Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu 65 70 75 80

Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly
85 90 95

Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp 100 105 110

Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr 115 120 125

Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp 130 135 140

Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro 145 150 155 160

Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu 165 170 175

Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys 180 185 190

Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr Tyr 195 200 205

Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val 210 215 220

Thr Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His 225 230 235 240

Thr His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu

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Ser Ser Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro
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tggcctgggc gggactgggg agtggcgagc cctcagatgc tgcatataag cagcagctgc 240
ttttgcccc
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ggactgctga cagcgagatt tctacaaggg actttccgct ggggactttc cagggaggtg 180
tggcctgggc gggactgggg agtggcaagt gaaagtgaaa gtgaaagtga gagccctcag 240
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      promoter construct
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ccatagtece geceetaact eegeceatee egeceetaac teegeceagt teegeceatt 180
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<212> DNA
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His His His His His
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